

SEQUENCE LISTING

<110> Grainger, David J.
 Tatalick, Lauen Marie
 Kanaly, Suzanne T.

<120> Compounds and methods to inhibit or augment an inflammatory response.

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<141> 1998-09-11

<150> US 08/927939

<151> 1997-09-11

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Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu

5 40 4

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Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala 35 40 45

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe 50 55 60

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35 40 45

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe 50 55 60

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 Ser
 Tyr
 Arg
 Cys
 Pro
 Cys

 Arg
 Phe
 Phe
 Glu
 Ser
 His
 Val
 Ala
 Arg
 Ala
 Asn
 Val
 Lys
 His
 Leu
 Lys

 Ile
 Leu
 Asn
 Thr
 Pro
 Asn
 Cys
 Ala
 Leu
 Gln
 Ile
 Val
 Ala
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 Leu
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85

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Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe 35 40 45

Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr 50 55 60

Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
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Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala 85 90 95

Glu Asn Ser

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100

<400> 25

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Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val

Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys
65 70 75 80

Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg 85 90 95

Ser Glu Pro Thr Thr Leu Phe Lys Thr Ala Ser Ala Leu Arg Ser Ser

Ala Pro Leu Asn Val Lys Leu Thr Arg Lys Ser Glu Ala Asn Ala Ser 115 120 125

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Val Thr Val Asn

145

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347

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His Leu Gly Arg Lys Ala His Thr Leu Lys Thr 90 95

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Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser	
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Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn	
30 35 40	

256

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Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile

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Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys	Arg	Phe	
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50

45

Lys Met

55

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Val Arg Met Arg Ala Ile Gly Lys Leu Glu Ile Ile Pro Ala Ser Leu	
40 45 50 55	

tcc tgc cca cgt gtt gag atc at gtgagtacaa gcccacctgc cgataaacgt Ser Cys Pro Arg Val Glu Ile Ile 60	2825
ccctccgta accacagt aaataagtga gggaaaccag gaaagatggg gacgggtctg tgactctaac taaggcacag tgcctgaact ctgacatgga cctgcagggc catcagctct gttggcctga cgttaatctg agtatctcac tcttatttct atag t gcc acg atg Ala Thr Met 65	2885 2945 2999
aaa aag aat gat gag cag aga tgt ctg aat ccg gaa tct aag acc atc Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys Thr Ile 70 75 80	3047
aag aat tta atg aaa gcg ttt agc caa aaa ag gtaggtttga tgttgctttt Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg 85 90	3099
tcaggaaatg gtggtctggg gagcagcgcc tgccctgggc tttgctgtgg gcatctgccc	3159
taaactcatg gcaccggcat gtgcctttgt ctctccattt acacagacac tgaggtgcct	3219
tottaggtca tacattocta gtgtotagaa gtggagcagt tattatacot gtcacgggta	3279
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Ser Lys Arg Ala Pro	
95	
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Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu Arg Val Ala Leu	
5 10 15 20	
ctg ctc ctg ctc ctg gtg gcc gcc agc cgg cgc gca gca gga gcg ccc	150
Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala Ala Gly Ala Pro	
25 30 35	
ctg gcc act gaa ctg cgc tgc cag tgc ttg cag acc ctg cag gga att	198
Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln Gly Ile	
40 45 50	
cac ctc aag aac atc caa agt gtg aag gtg aag tcc ccc gga ccc cac	246
His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly Pro His	
55 60 65	
tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat ggg cag aaa gct	294
Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln Lys Ala	

70 75 80

tgt etc aac ecc gea teg ecc atg get aag aaa acc acc gaa aag acg	342
Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu Lys Met	
85 90 95 100	
ctg aaa aat ggc aaa tcc aac tgaccagaag gaaggaggaa gcttattggt	393
Leu Lys Asn Gly Lys Ser Asn	
105	
ggctgttcct gaaggaggcc ctgcccttac aggaacagaa gaggaaagag agacacagct	453
gcagaggcca cctggattgc gcctaatgtg tttgagcatc acttaggaga agtcttctat	513
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Met Ser Leu

115

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ctg	tcc	agc	cgc	gcg	gcc	cgt	gtc	ccc	ggt	cct	tcg	agc	tcc	ttg	tgc	163
Leu	Ser	Ser	Arg	Ala	Ala	Arg	Val	Pro	Gly	Pro	Ser	Ser	Ser	Leu	Cys	
	5					10					15					
gcg	ctg	ttg	gtg	ctg	ctg	ctg	ctg	ctg	acg	cag	cca	ggg	ccc	atc	gcc	211
Ala	Leu	Leu	Val	Leu	Leu	Leu	Leu	Leu	Thr	Gln	Pro	Gly	Pro	Ile	Ala	
20					25					30					35	
agc	gct	ggt	cct	gcc	gct	gct	gtg	ttg	aga	gag	ctg	cgt	tgc	gtt	tgt	259
Ser	Ala	Gly	Pro	Ala	Ala	Ala	Val	Leu	Arg	Glu	Leu	Arg	Cys	Val	Cys	
				40					45					50		
tta	cag	acc	acg	cag	gga	gtt	cat	ccc	aaa	atg	atc	agt	aat	ctg	caa	307
Leu	Gln	Thr	Thr	Gln	Gly	Val	His	Pro	Lys	Met	Ile	Ser	Asn	Leu	Gln	
			55					60					65			
gtg	ttc	gcc	ata	ggc	сса	cag	tgc	tcc	aag	gtg	gaa	gtg	gta	gcc	tcc	355
Val	Phe	Ala	Ile	Gly	Pro	Gln	Cys	Ser	Lys	Val	Glu	Val	Val	Ala	Ser	
		70					75					80				
ctg	aag	aac	999	aag	gaa	att	tgt	ctt	gat	cca	gaa	gcc	cct	ttt	cta	403
Leu	Lys	Asn	Gly	Lys	Glu	Ile	Cys	Leu	Asp	Pro	Glu	Ala	Pro	Phe	Leu	
	85					90					95					
aag	g aaa	gtc	atc	cag	aaa	att	ttg	gac	ggt	gga	aac	aag	gaa	aac		448
Lys	Lys	Val	Ile	Gln	Lys	Ile	Leu	Asp	Gly	Gly	Asn	Lys	Glu	Asn		
100)				105					110						
															ttttct	508
															tatttg	568
att															ggaaaa	628
		tta	qcgc	ttaa	gc t	ttca	gctc	a gc					gca	tagt	acctct	688
cct																
cct gct	attt	gct	gtta	tttt	at c										agtgtg	748
cct gct ago	attt	gct aat	gtta cact	tttt ggct	at c gt t	aatc	ttac	a aa	gtgt	cttg	gaa	ttgt	agg	tgac	tattat	808
cct gct ago ttt	attt cagg tcca	gct aat aga	gtta cact aata	tttt ggct tccc	at c gt t tt a	aatc agat	ttac atta	a aa a ct	gtgt gaga	cttg aggc	gaa tgg	ttgt gggt	agg tta	tgac atgt		

tgggaaatat tttaatgt	tt cttggggaat	atgttagaga	attcccttac	tcttgattgt	988
gggatactat ttaattat	tt cactttagaa	agctgagtgt	ttcacacctt	atctatgtag	1048
aatatatttc cttattca	ga atttctaaaa	gtttaagttc	tatgagggct	aatatcttat	1108
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aaaaa					1173
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Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala

10 15 20

cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc 150

Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser

25 30 35

agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc 198
Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
40 55 55

agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag 246
Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
60 65 70

gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa 294

Glu	Ile	Cys	Ala	Asp	Pro	Lys	Glu	Lys	Trp	Val	Gln	Asn	Tyr	Met	Lys	
			75					80					85			

cac	ctg	ggc	cgg	aaa	gct	cac	acc	ctg	aag	act	tgaactctgc	tacccctact	347
His	Leu	Gly	Arg	Lys	Ala	His	Thr	Leu	Lys	Thr			
		90					95						

407 gaaatcaagc tggagtacgt gaaatgactt ttccattctc ctctggcctc ctcttctatg 467 ctttggaata cttctaccat aattttcaaa taggatgcat tcggttttgt gattcaaaat gtactatgtg ttaagtaata ttggctatta tttgacttgt tgctggtttg gagtttattt 527 gagtattgct gatcttttct aaagcaaggc cttgagcaag taggttgctg tctctaagcc 587 cccttccctt ccactatgag ctgctggcag tgggttgtat tcggttccca ggggttgaga 647 gcatgcctgt gggagtcatg gacatgaagg gatgctgcaa tgtaggaagg agagctcttt 707 gtgaatgtga ggttgttgct aaattattgt ttattgtgga aagatgaatg caatagtagg 767 825

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<221> CDS

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<222> (2488)...(2575)

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atggctccat atttgggttg tttccacaga actctttccc agaaatgctt tttctaggtt 180
aatggctaca catattcta ggcacctgac atactgacac ccacctctaa agtatttta 240
tgatccacaa ctagcgttta acacagcgcc ccagtcactc cgagactaat aaatagacaa 300

atgactgaaa cgtgacctca tgctttctat tcctccagct ttcattgagt tcctttcctc	360
tgggaggact gggggttgtc tagccctcca cagcatcagc ccattgaccc tatccttgtg	420
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catgcataga ccaattettt ttttttttt tttttgagat ggagtttcae ttttgttgce	540
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cgattctcct gccctcagcc tcccgagtag ctgggattac aggcatgtgc caccacgcct	660
gactactttt gtatttttag tagagatgga gtttctcttt cttggtcagg ttggtctcaa	720
actectgace teaggtgate egeageeteg geeteecaaa gtgttgggat tacaggtgtg	780
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Met Gln	
1	
gtc tcc act gct gcc ctt gcc gtc ctc ctc tgc acc atg gct ctc tgc	1245
Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala Leu Cys	
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aac cag gtc ctc tct gca cca c gtgagtccat gttgttgttg tgggtatcac	1297
Asn Gln Val Leu Ser Ala Pro	
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•	1777
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Leu

get get gae acg ecg ace gee tge tge tte age tae ace tee ega	cag 2002
Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg	
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att cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag	tgc 2050
Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln	
45 50 55	
tcc aag ccc agt gtc at gtaagtgcca gtcttcctgc tcacctctag	2097
Ser Lys Pro Ser Val Ile	
60	
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aacaggaaga aggaggcagc aggacactct gagggccccc ttgcctggag tcac	
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Phe Leu Thr Lys Arg Gly	/ Arg
65 70)
cag gtc tgt gct gac ccc agt gag gag tgg gtc cag aaa tac gtc	agt 2557
Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val	l Ser
75 80 85	
gac ctg gag ctg agt gcc tgaggggtcc agaagcttcg aggcccagcg	2605
Asp Leu Glu Leu Ser Ala	
90	
acctcagtgg gcccagtggg gaggagcagg agcctgagcc ttgggaacat gcg	
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5 10 15

cta ggg acc aag act gaa tcc tcc tca cgg gga cct tac cac ccc tca 153
Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro Ser
20 25 30

gag tgc tgc ttc acc tac act acc tac aag atc ccg cgt cag cgg att

Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg Ile

35

40

45

atg gat tac tat gag acc aac agc cag tgc tcc aag ccc gga att gtc 249

Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val

50 55 60 65

ttc atc acc aaa agg ggc cat tcc gtc tgt acc aac ccc agt gac aag 297

Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp	Lys
				70					75					80	

	_									gag Glu		tgagtga	iccc	343
			85					90						
														400
agaa	aggg	gtg 9	gcgaa	aggca	ac ag	gete	agaga	a cat	taaaq	gaga	agat	gccaag	gcccctcc	t 403
ccad	cca	ccc (ctaa	ctct	ca go	ccca	agtca	a cc	ctct	tgga	gcti	tccctgc	tttgaatta	ıa 463

481

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<221> CDS

<222> (2149)...(2260)

<221> CDS

<222> (3383)...(3482)

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Met Gln Ile Ile 1 acc aca gcc ctg gtg tgc ttg ctg cta gct ggg atg tgg ccg gaa gat Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met Trp Pro Glu Asp 5 10 15 20 gtg gac agc aag agc a gtgagttgg caggcatcat tttgcttct tctggggagg 1000 Val Asp Ser Lys Ser 25 gcagaaacgt ggtcagccac tctggggttg gagcagctt ctccttgaac tcaccaactc tatctccct tttctacct aaagagagag attgggaac ttggagcaac ttggagagg 1120 gctagtagga gaaccatgag ttggggcaaa cacaggaact ttggacagg tggggtgagg 1120 gctagtagga gaaccatgag ttggggcaaa cacaggaac tgaactgaa ggttcagtac tggggagg 1120 gggaggccc aaggtccag gaccacag ggtgagactt ctaccagtg aaggacttat tggggaggcc aaggaccta gaccaagg aggaacct tatgggaggcc aaggtcaag ggacagctg ggtgagct ctacatgtag aggagacca aggagctaca ctatttgga aaggagcaca ctattt 1360 agctctcaaa ctatatttc tctatcagt aacattggt accatttgga aagtacacca 1480 aggaggaagaa gctgggattg gaatgcagg tctttgggg aggtgaaac gggaggagaa ggagagaac gggaggagaa gggagagaa ggaggagaa ggaggagaa caagagaac gggaggagaa ggaggagaa ggagagaag ggaggagaa ctaaggacca gggaggagag 1600 ggattcaaa ctctatttt tctatcagt aattcttggg aagtgattc ctttgtatct fl660 catcagtttg gactcctcga acaattccta atcttccca gactaagacc ggacgagag 1720 gaccacagt tcctgcatca gactaaccag gtccccaagg ttgggggtc agaacgtg tggagaatg 1720 gaccactgtt tcctgcatca gactaaccag gtccccaagg ttgggggtc aagagcctttg tgaactgtg 1720 gaccactgtt tcctgcatca gactaaccag gtccccaagg ttgggggtc agaacctg ggatgaact 1780 ggacatgaata ctggggcaga accatgcaca ttgtggtgaa aaccaacaact ggatgagcct 1780 gacatgaata ctggggcaga accatgcaca tgtggtgaa aaccaacaac ggatgagcct 1780 ggacatgata ctcagggcc accagcaca tgtggtgaa aaccaacaac ggatgagcct 1780 ggacatgat ctccaagaa agtttattt tacagatggg aagtcagg caagggtgaa 1900 ggacatctt ctcaggcc accagcaca gggggggga ggggggaa gctgaacatct gaggcaacaaca 1960 ctcttgact tttacctagc cccaaaaa agtttattt tacagatgg ggggggagaacact tgtggtgaac tagacccaat 1960 ctcttgact tttacctag cccaagaacaa ggtggtga gaaatggag caacaccaat 1960 ctcttgat gtggtccca agcaggtgg gaaggtga gaaatggag ggggggaacatct tttacctag gacgaggtga agcaggtga agcaggtga ggaaggtga ggaagcatg ggggggga gctgttttt tgtttgtttt 2080 t		840
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30 35

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Asp Thr Val Gly Trp Val Gln Arg His Arg Lys Met Leu Arg His Cys	
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Pro Ser Lys Arg Lys

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Ile	Ala	Thr	Leu	Lys	Asp	Gly	Arg	Lys	Ile	Cys	Leu	Asp	Pro	Asp	Ala	
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1 5 10

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1 5 10

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Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp 35 40 45

Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile 50 55 60

Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala 70 75 80

Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys 85 90 95

Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
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Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
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<213> Homo sapiens

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<211> 93

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<213> Homo sapiens

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Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg

Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
50 55 60

Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp 65 70 75 80

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<212> PRT

<213> Homo sapiens

<400> 49

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Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile 35 40 45

Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Ser Val Ile
50 55 60

Phe Leu Thr Lys Arg Gly Arg Gln Val Cys Ala Asp Pro Ser Glu Glu 65 70 75 80

Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala 85 90

<210> 50

<211> 98

<212> PRT

<213> Homo sapiens

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Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu 35 40 45

Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile 50 55 60

Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys 65 70 75 80

Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu 85 90 95

Lys Thr

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Lys Val Ser Ala	a Ala Leu Lev	ı Trp Leu	Leu Leu	Ile Ala Al	a Ala Phe	
5		10		1	5	
agc ccc cag gg	g ctc gct ggg	g cca gct	tct gtc	cca acc ac	c tgc tgc	152
Ser Pro Gln Gl	y Leu Ala Gly	Pro Ala	Ser Val	Pro Thr Th	r Cys Cys	
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ttt aac ctg gc	c aat agg aag	g ata ccc	ctt cag	cga cta ga	g agc tac	200
Phe Asn Leu Al	a Asn Arg Ly	s Ile Pro	Leu Gln	Arg Leu Gl	u Ser Tyr	
35	4	ס		45		
agg aga atc ac						248
Arg Arg Ile Th	r Ser Gly Ly	s Cys Pro	Gln Lys	Ala Val Il	e Phe Lys	
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acc aaa ctg gc	c aag gat at	c tgt gcc	gac ccc	aag aag aa	g tgg gtg	296
Thr Lys Leu Al	a Lys Asp Il	e Cys Ala	Asp Pro	Lys Lys Ly	s Trp Val	
	70		75		80	
cag gat tcc at						344
Gln Asp Ser Me	t Lys Tyr Le	u Asp Gln	Lys Ser	Pro Thr Pr	o Lys Pro	
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ttcttacaat gca						464
atatatatat ata						524
taaaacttat cct						584
ttaccccctg gga						644
tctcttcctc cct						704
ttgttcttgt gaa						764
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<400> 52

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<210> 53

<211> 107

<212> PRT

<213> Homo sapiens

<400> 53

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Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile 85 90 95

Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn

100 105

<210> 54

<211> 98

<212> PRT

<213> Homo sapiens

<400> 54

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Ser Gly Thr Gln Gly Ile Pro Leu Ala Arg Thr Val Arg Cys Asn Cys 20 25 30

Ile His Ile Asp Asp Gly Pro Val Arg Met Arg Ala Ile Gly Lys Leu
35 40 45

Glu Ile Ile Pro Ala Ser Leu Ser Cys Pro Arg Val Glu Ile Ile Ala 50 55 60

Thr Met Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys
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Thr Ile Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg Ser Lys Arg 85 90 95

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<212> DNA

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<222> (18)...(338)

<400> 55

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ASII	FIO	AL 9	15	ДСИ	*** 9	• • •		20					25			
			10													
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	•	30					35					40				
cag	tgc	ttg	cag	acc	ctg	cag	gga	att	cac	ccc	aag	aac	atc	caa	agt	194
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Ile	Val	Lys	Lys	Ile	Ile	Glu	Lys	Met	Leu	Asn	Ser	Asp	Lys	Ser	Asn	
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tgt	cagt	tgt	tatt	tatt	ga a	atga	tttc	a ca	gtgt	gtgg	tca	acat	ttc	tcat	gttgaa	878
act	ttaa	gaa	ctaa	aatg	tt c	taaa	tatc	c ct	tgga	catt	tta	tgtc	ttt	cttg	taaggc	938

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<211> 93

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Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys 60 55

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln 80 75 70 65

Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met

90 85

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<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

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Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr 40 35

Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser 60 55

Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn

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65

308

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Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys

60

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Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro	Lys	Glu	Asn	Trp	Val	
70					75					80					85	
cag	agg	gtt	gtg	gag	aag	ttt	ttg	aag	agg	gct	gag	aat	tca			398
Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala	Glu	Asn	Ser			
				90					95							

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<210> 59

<211> 15

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<400> 59

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1 5 10 15

<210> 60 <211> 14 <212> PRT <213> Homo sapiens <400> 60 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala 10 5 <210> 61 <211> 15 <212> PRT <213> Homo sapiens <400> 61 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val 15 10 5 <210> 62 <211> 15 <212> PRT <213> Homo sapiens <400> 62 Glu Ser Tyr Arg Arg Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala 15 10 1 <210> 63 <211> 15 <212> PRT

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<210> 64

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<400> 63

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<400> 73

Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys

1 5 10

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Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln

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Leu Cys Leu Leu Leu Ile Ala Ala Thr Phe Ile Pro Gln Gly Leu Al	
20	-
10 15 20	
	c 148
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Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe Th	.r
25 30 35	
aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc ac	c 196
Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile Th	ır
	55
agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg gc	ec 244
Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val Al	
60 65 70	
aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc at	.g 292
Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser Me	
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	_ 241
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Met Asn Ala Lys Val Val Val Leu Val Leu	
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Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser	
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Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile	
45 50 55	
43	
gta gcc cgg ctg aag aac aac aga caa gtg tgc att gac ccg aag	304
Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys	
60 65 70 75	
cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag	346
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys	
80 85	

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Val	Ile	Leu	Ile	Ala	Thr	Ala	Leu	Cys	Ala	Pro	Ala	Ser	Ala	Ser	Pro	
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Tyr	Ser	Ser	Asp	Thr	Thr	Pro	Cys	Cys	Phe	Ala	Tyr	Ile	Ala	Arg	Pro	
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90																
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															aggcag	649
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															aaatac	769

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		agactccgtc				949
		gaggcgctgc				1009
		tgcaagggct				1069
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Met Lys Leu

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Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala Phe Cys Ser

5 10 15

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Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys

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Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr

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45

50

tat gag acc agc agc ctc tgc tcc cag cca gct gtg gta ttc caa acc

Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr

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Glu Tyr Val Tyr Asp Leu Glu Leu Asn	
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Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn	
1 5 10 15	
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Val Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg	
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Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Gln	

35 40 45

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Ser	Met	Lys	His	Leu	Asp	Gln	Ile	Phe	Gln	Asn	Leu	Lys	Pro				
	65					70					75						
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	М	et Lys Ala	Ser Ala Ala	Leu Leu	
		1	5		

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10 15

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пуъ	цуъ	110	110	45	01	5			50	•	_			55		
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OIU	110	C _I D		F				-	_							
		75					80					85				
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His	Leu 90	gac Asp	aag Lys	Lys	Thr	Gln 95	act Thr	Pro	Lys	Leu		acat				645 705
His gaa	Leu 90 aaca	gac Asp agc	aag Lys catg	Lys actt	Thr ga g	Gln 95 aaac	act Thr	Pro a at	Lys ttgt	Leu atac	cct	acat gtcc	ttt	ctca	gagtgg	
His gaa ttc	Leu 90 aaca tgag	gac Asp agc att	aag Lys catg	Lys actt taat	Thr ga g ct a	Gln 95 aaac attc	act Thr aaat taag	Pro a at g aa	Lys ttgt tatg	Leu atac agct	cct tta	acat gtcc tgta	ttt ata	ctca atgt	gagtgg gaatca	705
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gaa ttc tgg tgg gca taa	Leu 90 aaca tgag tttt tggg atgo aaga	gac Asp agc att tct ttt ttcc tttt	aag Lys catg attt tagt tgaa tccc gctt	Lys actt taat agat cata	Thr ga g ct a tt t aa g ct a ttg t	Gln 95 aaac attc aaaa cctt cctc taag	act Thr aaat taag gtta ggat atgg	Pro a at g aa t ta g ta g gg	Lys ttgt tatg atat tatg tatt	Leu atac agct ttta tcat gtat	cct tta att ctc aag	gtcc tgta taat agtg tcct	ttt ata .ctt gctg :tgc	ctca atgt ccat taaa aaga tgtt	gagtgg gaatca ggattt aactgt	705 765 825 885 945 1005

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						1				5					10	
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Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile 50 55 60

Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys 65 70 75 80

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<223> A chemokine peptide variant

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Lys Arg Phe Lys

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